

Table SI. Primer sequences used for circRNA.

circRNA	Primer	Sequence (5'-3')	Gene name	Length, bp	Best transcript ^a	Position	Strand
hsa_circ_0006137	Forward	TTGTGCTGTGACGGGTAGAC	BAZ1A	145	NM_013448	chr14:35331249-35331528	-
	Reverse	TAAGCGCGAACGATGGGTAA					
hsa_circ_0079422	Forward	AGGCCCTCTGCTTTTCTTCC	ICA1	120	NM_004968	chr7:8257934-8275635	-
	Reverse	GGTTCACCGTCAGCCAAGTA					
hsa_circ_0007375	Forward	TGGCGGAATACAGCAAGACA	FBXL13	116	NM_145032	chr7:102665509-102669865	-
	Reverse	TCTGCAGCAGCTCTTTTGAGT					
hsa_circ_0005597	Forward	GTGGGGACTGCAAAGCAAAG	PITPNB	232	NM_012399	chr22:28249524-28256229	-
	Reverse	CTGACCCTACAGGGGACTCA					
hsa_circ_0006961	Forward	AGAGGCGTCCTTAGCAGAGA	BRAF	179	NM_004333	chr7:140494107-140508795	-
	Reverse	ATCGGTCTCGTTGCCCAAAT					
hsa_circ_0004305	Forward	TGTGGTGGTGATCTGAGTCTTG	TTN-AS1	334	NR_038272	chr2:179400458-179407088	+
	Reverse	GTCACACCAAAAACACCATTGAG					
hsa_circ_0002775	Forward	CCTGCTGCTCCACCTACAAA	GPBP1	224	NM_022913	chr5:56542126-56545403	+
	Reverse	TTGGTTAGACGAGGCTGCTG					
hsa_circ_0009096	Forward	TCCTGTCAGCGGGAATTGAC	UTRN	131	NM_007124	chr6:144772505-144780490	+
	Reverse	AGAAAGCTATCGAAGCCCCG					
hsa_circ_0085616	Forward	AGAAATGGATGCCGACCAG	ASAP1	73	NM_001247996	chr8:131370262-131374017	-
	Reverse	GTGGGCGAGTTGTAGTCCTC					
hsa_circ_0026229	Forward	ACAGTATGCCTCCCCAGTCT	LARP4	136	NM_052879	chr12:50821544-50848200	+
	Reverse	ATTGGGAAAGGGAGCCAGTG					
hsa_circ_0005654	Forward	ACCCACTCTGAGGAGAGACC	PRDM5	126	NM_018699	chr4:121675707-121732604	-
	Reverse	ATCGCAGTGATGGCACTTGA					
hsa_circ_0004692	Forward	CTCTTCTGCCTATGAGCGGG	SETD2	302	NM_014159	chr3:47079155-47108608	-
	Reverse	CAGCATTAGGGTTGCTGGGA					
hsa_circ_0023936	Forward	ATCCACAGTTGGCAGACAG	PICALM	297	NM_007166	chr11:85718584-85742653	-
	Reverse	TCCATCAGCCCCTCTCTTCA					
hsa_circ_0004383	Forward	GACACTGGTGCAGGTAGCTC	ZNF292	115	NM_015021	chr6:87920168-87928449	+
	Reverse	AGTGCACAGTACCGGGTTTT					
hsa_circ_0002822	Forward	ACGAGCCAGTGCATGAAAGA	C2orf67	333	NM_152519	chr2:210993754-211019335	-
	Reverse	ATGCTTTGCCAGGAGCATCT					
hsa_circ_0008777	Forward	TCTTCCCAGCGCATTCTTT	AURKA	91	NM_198433	chr20:54956488-54961589	-
	Reverse	TGGTTGCCTGCAATTGCTTC					
hsa_circ_0081171	Forward	ACCTTTGAGACTGCAAGGCA	SGCE	151	NM_001099401	chr7:94248069-94259153	-
	Reverse	TCACTGCGCCAAGAAAGTCT					
hsa_circ_0084665	Forward	AGAGGAGGACAGATACCGACA	CSPP1	132	NM_024790	chr8:68007527-68007967	+
	Reverse	GGAATGCCAGCCTTGCTTG					
hsa_circ_0075828	Forward	CTGCATTACTGCTCAACCACA	LINC00340	89	NR_015410	chr6:22020567-22020771	+
	Reverse	CCCAGGGATGACTTGGTGAC					
hsa_circ_0000374	Forward	GAGATGGGTGTCGTGAGCTG	ITFG2	103	NM_018463	chr12:2929251-2930958	+
	Reverse	AGCTGCCCTGTCAGATGTTT					
hsa_circ_0006460	Forward	AGACGGGACTCGAGTGATGA	BRAF	158	NM_004333	chr7:140476711-140494267	-
	Reverse	AACTGCTGAGGTGTAGGTGC					

hsa_circ_0005934	Forward	TGGCAGATTTTGGAGTGGCT	STK3	123	NM_006281	chr8:99718694-99735197	-
	Reverse	CGGCCACACAGTTATAGCCT					
hsa_circ_0001747	Forward	AAAGCTCGAAAGGCCTGCTA	MKLN1	240	NM_013255	chr7:131071878-131084192	+
	Reverse	CCCCAGGACAAGAGTGGAAC					
hsa_circ_0054345	Forward	GGTGACTGGCAAAGAGCTGA	LRPPRC	188	NM_133259	chr2:44139570-44145537	-
	Reverse	GTGGTTGAGGCTGACGAAGA					
hsa_circ_0067991	Forward	AACAGAGCGACGAGCAAGAA	FNDC3B	385	NM_022763	chr3:171969049-172025291	+
	Reverse	GGTGGTGAAGCTAACAGGCT					
hsa_circ_0005047	Forward	TTGATTCCTCGTGCCAGACC	CREB3L2	332	NM_194071	chr7:137586099-137600758	-
	Reverse	AGCGATCAGGGTCTCTTCT					
hsa_circ_0008177	Forward	ACCCCTTGGAAGAGGACTGT	FAM13B	269	NM_016603	chr5:137288316-137290065	-
	Reverse	ATCACTGTAGGAGGGCTTGC					
hsa_circ_0003526	Forward	TTCCGGCAGATTTTGGCTCT	SPG21	168	NM_016630	chr15:65266939-65275931	-
	Reverse	GGCCAAAAGCCTCCCAAAG					
hsa_circ_0056744	Forward	AAGCCCGTGAACGTGAAAGA	PRPF40A	96	NM_017892	chr2:153519116-153525784	-
	Reverse	TCGGAGGAGCAGCTTGTTTT					
hsa_circ_0008523	Forward	TAATTGCACAGGCACGGACA	DDX21	89	NM_004728	chr10:70723046-70726959	+
	Reverse	CCTGTCTTGCAGTTCCCAT					
hsa_circ_0002338	Forward	ACACATCTTCCCATGGCAG	ALAS1	429	NM_000688	chr3:52238708-52240767	+
	Reverse	TGCAGCAGTTCTCTGAGGTG					
hsa_circ_0088088	Forward	GGCTGGCAGGATGTACAGTT	HSDL2	375	NM_032303	chr9:115166274-115171301	+
	Reverse	CAAGGTAGGTGCCTCTGGTG					
hsa_circ_0008932	Forward	GAGGGTCTGCGTGAAATCCA	LRP6	512	NM_002336	chr12:12332743-12340053	-
	Reverse	CGATCAGTGCCAGTGTCTGT					
hsa_circ_0001383	Forward	TCTCCAGCCAGATACTCCCC	DLG1	97	NM_001204387	chr3:196842797-196846401	-
	Reverse	CCGTTGAGCCACGATGAAGA					
hsa_circ_0002485	Forward	ACCAGCTGGAGGATGAGTCT	ATP9B	238	NM_198531	chr18:76856475-76886375	+
	Reverse	AGCCATACTGTGCGAGCTTT					
hsa_circ_0055019	Forward	GTCAGCTGCGAATCAAACCG	APLF	296	NM_173545	chr2:68717321-68753374	+
	Reverse	TCCTTCCAGTTGTGAGGCAC					
hsa_circ_0061286	Forward	CAGGGCATTGAGGAGACTG	USP25	164	NM_013396	chr21:17150222-17177577	+
	Reverse	CGGGAGCTTTGTCTGTCTT					
hsa_circ_0003113	Forward	TGCAACTCCTATCACCAGCTC	RYK	720	NM_001005861	chr3:133876964-133914026	-
	Reverse	AAGGCCACACATCACTAGC					
hsa_circ_0000690	Forward	CATCATCACGGATGGGGAGG	ITGAL	123	NM_001114380	chr16:30495147-30495584	+
	Reverse	TTGTGGAGGGTCTCCTGACT					
hsa_circ_0004173	Forward	TGCTGCTGAAATCCTTGGGA	RAB28	401	NM_004249	chr4:13338516-13383218	-
	Reverse	CCTGCCACTGTGAGGCAATA					
hsa_circ_0070942	Forward	CTGGAGGAGATCGAACAGGC	LARP1B	554	NM_018078	chr4:129042980-129100667	+
	Reverse	AGGGGGATTTGTGCTATGCC					
hsa_circ_0006355	Forward	TGCTAATACCGTGATGCGCT	TMLHE	763	NM_018196	chrX:154736558-154766779	-
	Reverse	GACTGGCCCAATCCCAATCA					
hsa_circ_0054618	Forward	TAAGGCAGCGGTCCCAGATA	CCDC88A	525	NM_001135597	chr2:55559701-55562300	-
	Reverse	TCAGGAGCTCCAAACCCTTC					
hsa_circ_0082002	Forward	CAGTCGGAGGTTCACTGCAT	MET	595	NM_001127500	chr7:116339124-	+

	Reverse	AATCTGGCTTGCTTTGTGCG				116340338	
hsa_circ_0008585	Forward	AGTGGCACACAGAGTTCTCG	BIRC6	212	NM_016252	chr2:32832521-32836649	+
	Reverse	GTCCTGCCTACCCGCTTATC					
hsa_circ_0008366	Forward	TAACCGAATGTTCCCGAGCC	RIC8B	127	NM_018157	chr12:107219503-107254190	+
	Reverse	AGGCGCACCAGCTTATTTCT					
hsa_circ_0017160	Forward	CTCCGAGGAATGGAAGCCA	MTR	81	NM_000254	chr1:237013643-237016388	+
	Reverse	CCCATGTCCATGCCAGACTT					
hsa_circ_0067323	Forward	TGAGGACCTGATCCTGGAG	TMCC1	313	NM_001017395	chr3:129546645-129551669	-
	Reverse	CTGGGTGGCACTCGAATCT					
hsa_circ_0005406	Forward	GGTCCTGGACAGTGTGGAAG	PHACTR4	73	NM_001048183	chr1:28785595-28793046	+
	Reverse	GCCAAAGCCTGAGAACTTGC					
hsa_circ_0007518	Forward	GTGGTGGTGTGCACATTGAG	NDUFB2	76	NM_004546	chr7:140402665-140404763	+
	Reverse	AACTCGCTCTGGAACACCTG					
hsa_circ_0003639	Forward	TTTACGAGGACTTGGAGCC	ZC3H11A	237	NM_014827	chr1:203786053-203787817	+
	Reverse	CACACCTGTCGAAAACAGCG					
hsa_circ_0032125	Forward	CGGGATCAACATCCCACACA	PRKCH	452	NM_006255	chr14:61909828-61924397	+
	Reverse	TCACGTCCTTCTTCAGCACC					
hsa_circ_0082415	Forward	ACTTCTGGGCGTACAGTGTG	MKLN1	536	NM_001145354	chr7:131113791-131130662	+
	Reverse	TCGCTGGCCACCAAATACAT					
hsa_circ_0027969	Forward	CCAGTGTTTGTGCGGTTCTG	SLC41A2	564	NM_032148	chr12:105255068-105322472	-
	Reverse	TGCCATGATGCCACTGGATT					
hsa_circ_0008006	Forward	ATGTTGCCAGAGAGGCAGATG	RPRD1B	97	NM_021215	chr20:36668836-36694658	+
	Reverse	TGTATGAACTCGCCGCCATA					
hsa_circ_0078299	Forward	GCTGGACAGGAAACGGAGAA	AKAP12	102	NM_005100	chr6:151669845-151674887	+
	Reverse	CACTGCGGTTGACTCTGACT					
hsa_circ_0004670	Forward	AAGGCTGGGTACATGACAGC	BAZ1B	482	NM_032408	chr7:72873865-72884813	-
	Reverse	TGAAATGACCCGGGCTTCAA					
hsa_circ_0004960	Forward	GCAGTGGAGACTCTTTGGA	NUP98	71	NM_016320	chr11:3794861-3797251	-
	Reverse	AAAGAGGGAGCCAGATGTGC					
hsa_circ_0009069	Forward	TCCAAATCTCGGCGAACCAA	PHF8	140	NM_015107	chrX:54013510-54014377	-
	Reverse	GTCGCCTTCTCCTTTCCCAA					
hsa_circ_0075748	Forward	GGCAGCAAGGAGTGAAAAC	KIF13A	250	NM_001105568	chr6:17772138-17779330	-
	Reverse	CTCTGGCCAACCCTTGTCAT					
hsa_circ_0020522	Forward	CAGCAGTAGCAAAGGGACCA	PPP2R2D	325	NM_018461	chr10:133753534-133761295	+
	Reverse	ACCGTTCCAGCAACTCAA					
hsa_circ_0007262	Forward	AGGCAGTCAGTCGGAAGTG	CHD2	123	NM_001271	chr15:93467550-93472321	+
	Reverse	TTGGAACCTGCTGATTCGCT					
hsa_circ_0006365	Forward	ATGGGTTGGGAAGATACCGC	TPST1	95	NM_003596	chr7:65751497-65751696	+
	Reverse	GTGGGTTGGCATATGGGTCA					
hsa_circ_0019607	Forward	CAAGTTGCACACAGTGGAGC	OGA	630	NM_012215	chr10:103552595-103570071	-
	Reverse	TCGTGACCGCCATTCTTCAA					
hsa_circ_0002220	Forward	AGCCAGCTGCAAGGAATCAA	MED13	365	NM_005121	chr17:60061531-60062451	-
	Reverse	GGGGCAGATATTGGCTTGGT					
hsa_circ_0006127	Forward	TTTCTGTACCCTGCCCCAAC	SRCAP	95	NM_006662	chr16:30740286-30740893	+
	Reverse	GGGCAGCCTCGGTATAAGTC					

hsa_circ_0001376	Forward	GCATGACATGGTGGCAACTC	ATP13A3	107	NM_024524	chr3:194169185-194175121	-
	Reverse	CCATGACATCTCCTGGCACA					
hsa_circ_0067480	Forward	CATGACAGGCAAGGGGAAGT	STAG1	254	NM_005862	chr3:136183722-136221621	-
	Reverse	TGTGCCGAGTACACCAAGTG					
hsa_circ_0072697	Forward	TCACCCATGTGGTATGCACC	PPWD1	485	NM_015342	chr5:64863339-64868113	+
	Reverse	AGGAGGCCAGTCCAGTATT					
hsa_circ_0084188	Forward	CACTGCAGGTCAGAAGAGCA	SPIDR	183	NM_001080394	chr8:48192449-48206619	+
	Reverse	TGGTGGTTTCTTGCTTGGGT					
hsa_circ_0003456	Forward	TACATCACCCGCTACATCGC	PSMA7	118	NM_002792	chr20:60714130-60716000	-
	Reverse	AGAGCCTAGGAGTGCCATCA					
hsa_circ_0000842	Forward	TGGAAAATGCAGCCTCAGGT	RPRD1A	154	NM_018170	chr18:33606862-33613800	-
	Reverse	GCCAGCAACATACACGCATC					
hsa_circ_0001979	Forward	GACTGGACCATCACTGCACA	SIPA1L1	613	NM_015556	chr14:72054287-72056087	+
	Reverse	GTCCATGCTGAGGCTTCCTT					
hsa_circ_0001771	Forward	CGGTCTGGAGAAGAAGAGC	RBM33	387	NM_053043	chr7:155457868-155473602	+
	Reverse	TGTCAACTCAGCTTCGTGGC					
hsa_circ_0004276	Forward	CTTGTGAATGGTCTGGGC	SUCLG2	81	NM_003848	chr3:67546221-67559327	-
	Reverse	TCCAAGAAGTTGGCTGGCTT					
hsa_circ_0014624	Forward	CCAGGAAGGCTTGAGACAG	GON4L	251	NM_001037533	chr1:155734790-155736500	-
	Reverse	CAGTGCTGCAGGAGACTCAA					
hsa_circ_0004179	Forward	GCCCTGTACACAGAAGCCAT	CLEC16A	111	NM_015226	chr16:11063017-11076848	+
	Reverse	GGCCTGGTTATCCACTGAGA					
hsa_circ_0077495	Forward	GGCAGAGAGATGCAGACGTT	ASCC3	181	NM_006828	chr6:101246588-101253756	-
	Reverse	AGTGGCATTGGTTCGCTGTA					

^aBioinformatics result obtained by comparing the head and tail chromosomal positions with known transcripts. circRNA, circular RNA; chr, chromosome; -, negative strand; +, positive strand.

Table SII. Clinical information of patients with biliary atresia.

No.	Sex	Surgery date	Age at surgery, days
242	Female	2018/6/8	46
243	Female	2018/6/8	44
250	Male	2018/6/15	108
D1916000091	Female	2018/3/30	99
D1916000231	Female	2018/4/20	100
D1916000471	Female	2018/7/25	65
D1916000601	Male	2018/8/3	86
D1916000641	Male	2018/9/11	55
D1916000951	Female	2018/12/26	65
D1916000981	Male	2019/1/9	148
D1916001301	Female	2019/5/17	48
D1916001361	Male	2019/6/19	48
D1916001391	Male	2019/7/3	108
D1916001641	Male	2019/10/9	38
D1916001691	Male	2019/10/30	54
D1916001701	Male	2019/11/4	120
D1916001781	Female	2019/11/15	77
D1916001821	Female	2019/11/27	42
D1916001901	Male	2019/11/29	67
D1916001911	Male	2019/12/17	137
D1916001961	Female	2020/2/17	97
D1916001991	Female	2019/12/27	96
D1916002001	Female	2019/12/31	62
D1916002011	Female	2019/12/31	62
D1916002031	Male	2020/2/6	70
D1916002041	Male	2020/2/6	70
D1916002081	Female	2020/3/23	85
D1916002091	Female	2020/3/24	79
D1916002111	Male	2020/3/20	82
D1916002131	Male	2020/3/9	54
D1916002151	Female	2020/3/6	57
D1916002161	Female	2020/4/13	37
D1916002181	Female	2020/4/10	45
D1916002201	Female	2020/4/14	80
D1916002261	Female	2020/4/22	50
D1916002271	Female	2020/4/27	45
D1916002331	Female	2020/5/14	66
D1916002341	Female	2020/5/14	66
Mean			72.58
SD value			27.31

Table SIII. Clinical information of choledochal cyst patients.

No.	Sex	Surgery date	Age at surgery, days
D1916000111	Female	2018/4/2	2323
D1916000141	Female	2018/4/9	604
D1916000171	Male	2018/4/18	98
D1916000181	Female	2018/4/18	1456
D1916000201	Female	2018/4/20	159
D1916000211	Male	2018/4/23	63
D1916000221	Female	2018/4/24	2721
D1916000241	Female	2018/4/25	1306
D1916000251	Female	2018/4/27	3570
D1916000261	Female	2018/3/2	209
D1916000271	Male	2018/5/2	4091
D1916000301	Female	2018/5/31	2105
D1916000311	Male	2018/5/17	131
D1916000321	Male	2018/5/23	122
D1916000371	Female	2018/5/31	2105
D1916000391	Female	2018/6/4	1329
D1916000401	Male	2018/6/11	1191
D1916000411	Female	2018/6/14	1794
D1916000421	Male	2018/6/15	590
D1916000441	Female	2018/7/4	1950
D1916000491	Male	2018/8/1	47
D1916000501	Female	2018/8/27	471
D1916000621	Female	2018/9/7	2842
D1916000691	Female	2018/9/29	31
D1916000701	Female	2018/9/30	995
D1916000721	Female	2018/10/10	1458
D1916000731	Female	2018/10/11	1435
D1916000741	Female	2018/10/17	1077
D1916000751	Female	2018/10/18	862
D1916000761	Male	2018/10/22	186
D1916000781	Female	2018/10/31	65
D1916000791	Female	2018/11/1	4337
D1916000801	Female	2018/10/15	1319
D1916000811	Male	2018/11/7	63
D1916000821	Female	2018/11/8	229
D1916000831	Female	2018/11/14	786
D1916000871	Female	2018/11/26	1407
D1916000881	Female	2018/11/28	1852
Mean			1209.70
SD value			1158.49